

FIG. 1

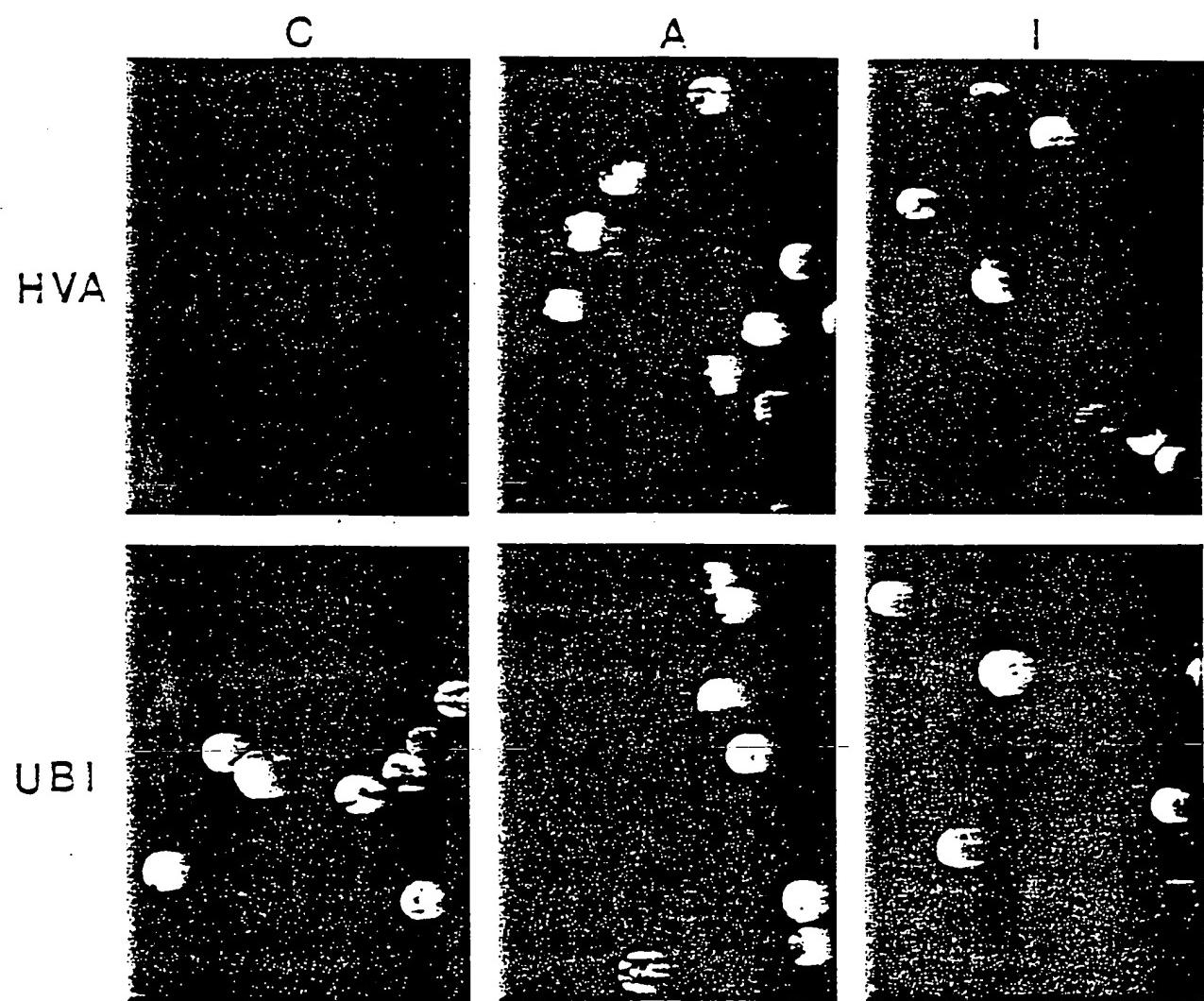


FIG.2

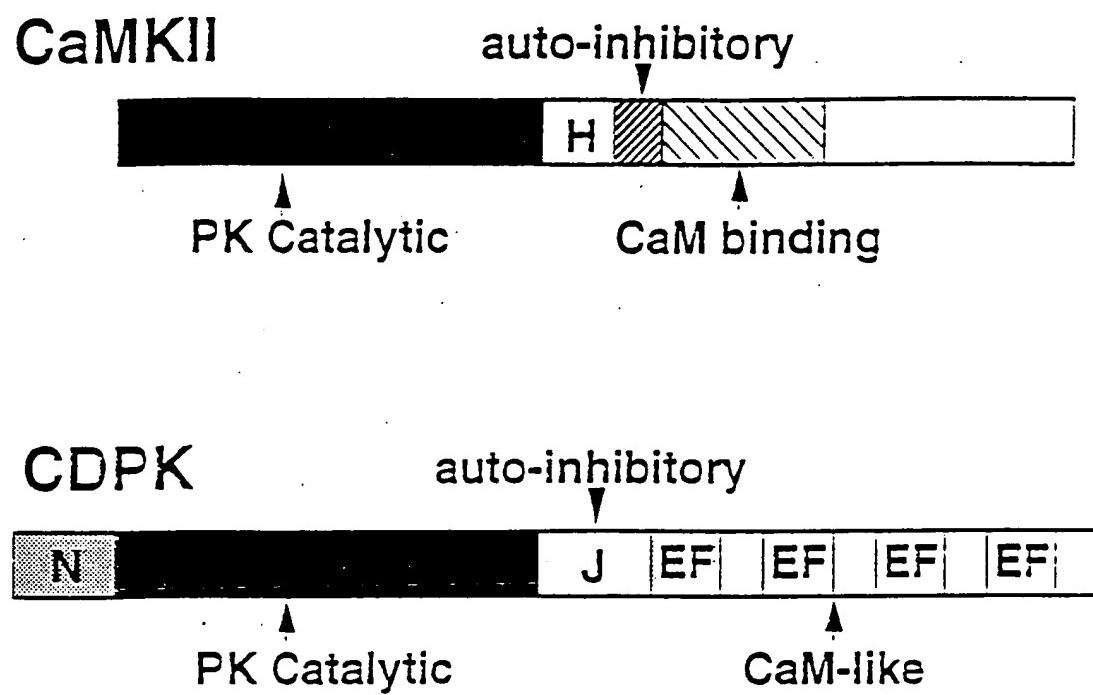


FIG. 3A

A C D P K T F G E Q V T F P K P G T

Acdpk	H C H T C V G P S R	H G F L Q S S V S A A	H W R P R D G D S S	A S H S H G D I A S S	E A V S G E H R S R	I S D E V Q H K P P	60
Acdpk1	0
Acdpk1a	0
Acdpk2	0
Acdpk	E Q V T F P K P G T	D V E T K D R E T R	T E S K P E T L E	I S T E S K P E T R	Q E T R S E T K P E	S K P D P P A K P K	120
Acdpk1	0
Acdpk1a	0
Acdpk2	0
Acdpk	R P K H H R R Y S S	A C I R T E S V L Q	R K T E E F P T E F	S H Q R K H G G	G E F G T T E H G V E	K T T G K E F A C I	179
Acdpk1	40
Acdpk1a	40
Acdpk2	55
Acdpk	6 T A K D K L I D	W E V E D P V R D E I V	O F V H H E A G I P	N V V I S T H G A V E	P V V A V H V Y E	C C A G G G E E L I P D F	219
Acdpk1	6 T S E K D L I D	W E V E D P V R D E I V	O F V H H E A G I P	N V V I S T H G A V E	P V V A V H V Y E	C C A G G G E E L I P D F	160
Acdpk1a	6 T S E K D L I D	W E V E D P V R D E I V	O F V H H E A G I P	N V V I S T H G A V E	P V V A V H V Y E	C C A G G G E E L I P D F	160
Acdpk2	6 T S E K D L I D	W E V E D P V R D E I V	O F V H H E A G I P	N V V I S T H G A V E	P V V A V H V Y E	C C A G G G E E L I P D F	175
Acdpk	T I Q R G C Q P T E R	K A A E L T F P T I V	G V V E A E E T S L Q	V Y Y H H P H P D E I E	F F E V S T U F D E	L H E T T H P F G H S	299
Acdpk1	T I Q R G C Q P T E R	K A A E L T F P T I V	G V V E A E E T S L Q	V Y Y H H P H P D E I E	F F E V S T U F D E	L H E T T H P F G H S	160
Acdpk1a	T I Q R G C Q P T E R	K A A E L T F P T I V	G V V E A E E T S L Q	V Y Y H H P H P D E I E	F F E V S T U F D E	L H E T T H P F G H S	160
Acdpk2	T I Q R G C Q P T E R	K A A E L T F P T I V	G V V E A E E T S L Q	V Y Y H H P H P D E I E	F F E V S T U F D E	L H E T T H P F G H S	175
Acdpk	W E F K P D D V F T	D V V G S F P V V V H M	R E V V F R K R G G P	E A P V V N S A G V I	V Y T H L S G V F P D	F F H E T E G G I F	359
Acdpk1	W E F K P D D V F T	D V V G S F P V V V H M	R E V V F R K R G G P	E A P V V N S A G V I	V Y T H L S G V F P D	F F H E T E G G I F	220
Acdpk1a	W E F K P D D V F T	D V V G S F P V V V H M	R E V V F R K R G G P	E A P V V N S A G V I	V Y T H L S G V F P D	F F H E T E G G I F	220
Acdpk2	W E F K P D D V F T	D V V G S F P V V V H M	R E V V F R K R G G P	E A P V V N S A G V I	V Y T H L S G V F P D	F F H E T E G G I F	235
Acdpk	E Q V T L H G D T D F	S S D P D V P S T S E P	S A A X S V K Q F L E	V K D P K K R H T Q A	V Q V L C H P H Y O	V D G V 411	
Acdpk1	E Q V T L H G D T D F	S S D P D V P S T S E P	S A A X S V K Q F L E	V K D P K K R H T Q A	V Q V L C H P H Y O	V D G V 411	
Acdpk1a	E Q V T L H G D T D F	S S D P D V P S T S E P	S A A X S V K Q F L E	V K D P K K R H T Q A	V Q V L C H P H Y O	V D G V 411	
Acdpk2	E Q V T L H G D T D F	S S D P D V P S T S E P	S A A X S V K Q F L E	V K D P K K R H T Q A	V Q V L C H P H Y O	V D G V 411	

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FIG. 3B

PK Constructs

	1 a.a. ATG	413 a.a.	TGA
1.	35SC4PPDK	ATCDPK (AK1)	DHA NOS
2.	35SC4PPDK	ATCDPK1	274 a.a. DHA NOS
3.	35SC4PPDK	ATCDPK1a	274 a.a. DHA NOS
4.	35SC4PPDK	ATCDPK2	289 a.a. DHA NOS
5.	35SC4PPDK	ATPKa	284 a.a. DHA NOS
6.	35SC4PPDK	ATPKb	283 a.a. DHA NOS
7.	35SC4PPDK	ASK1	265 a.a. DHA NOS
8.	35SC4PPDK	ASK2	265 a.a. DHA NOS

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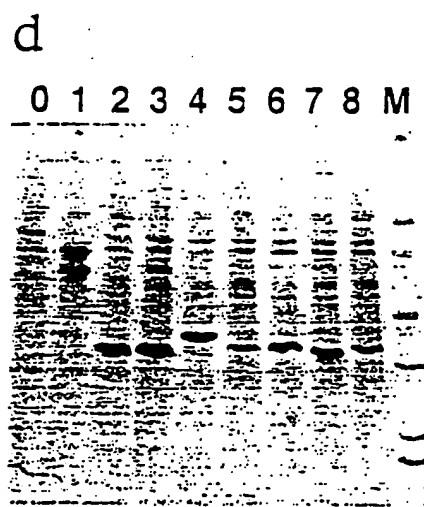


FIG. 3D

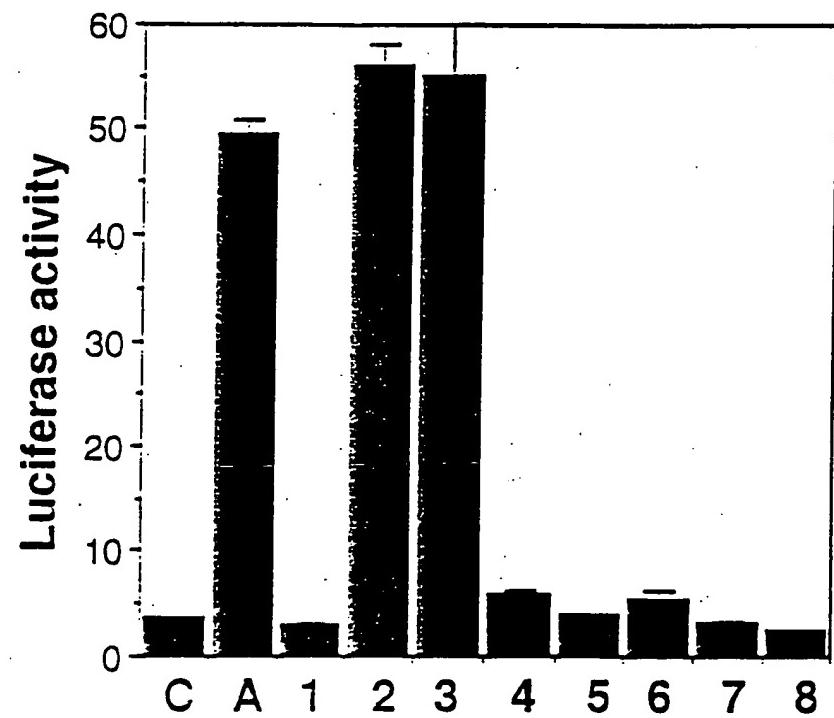
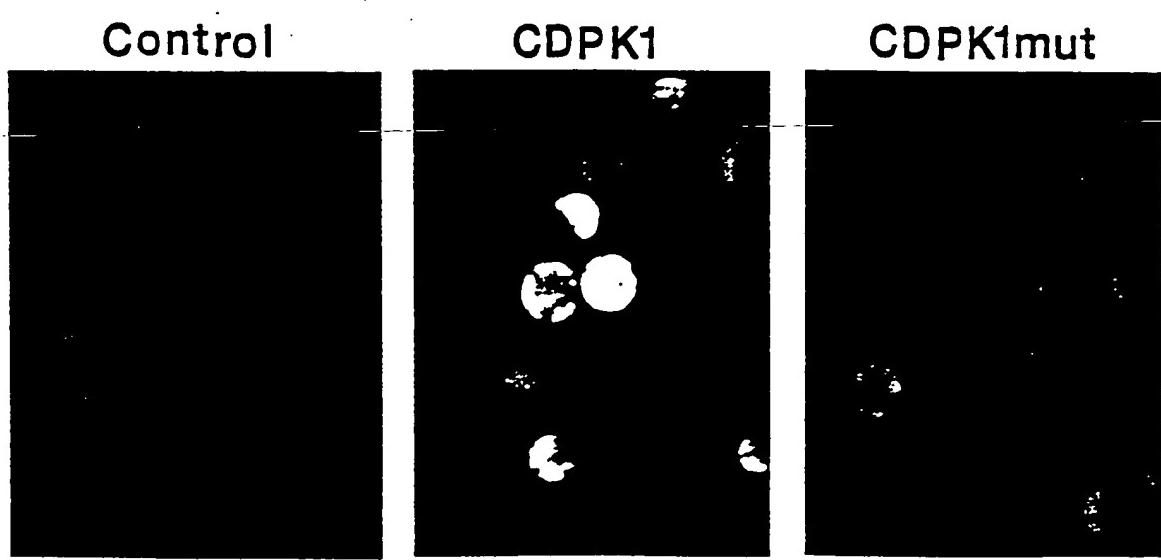


FIG. 3E



FIG. 4A



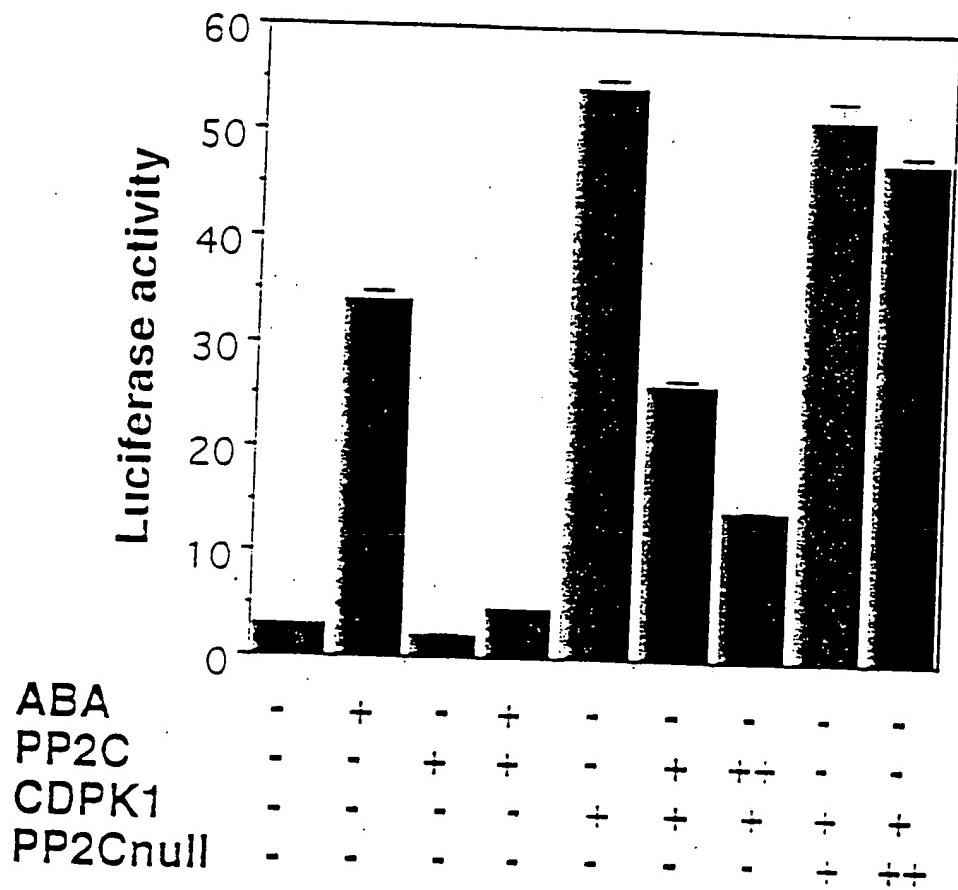


FIG. 4C

A model of stress signalling in plant cells

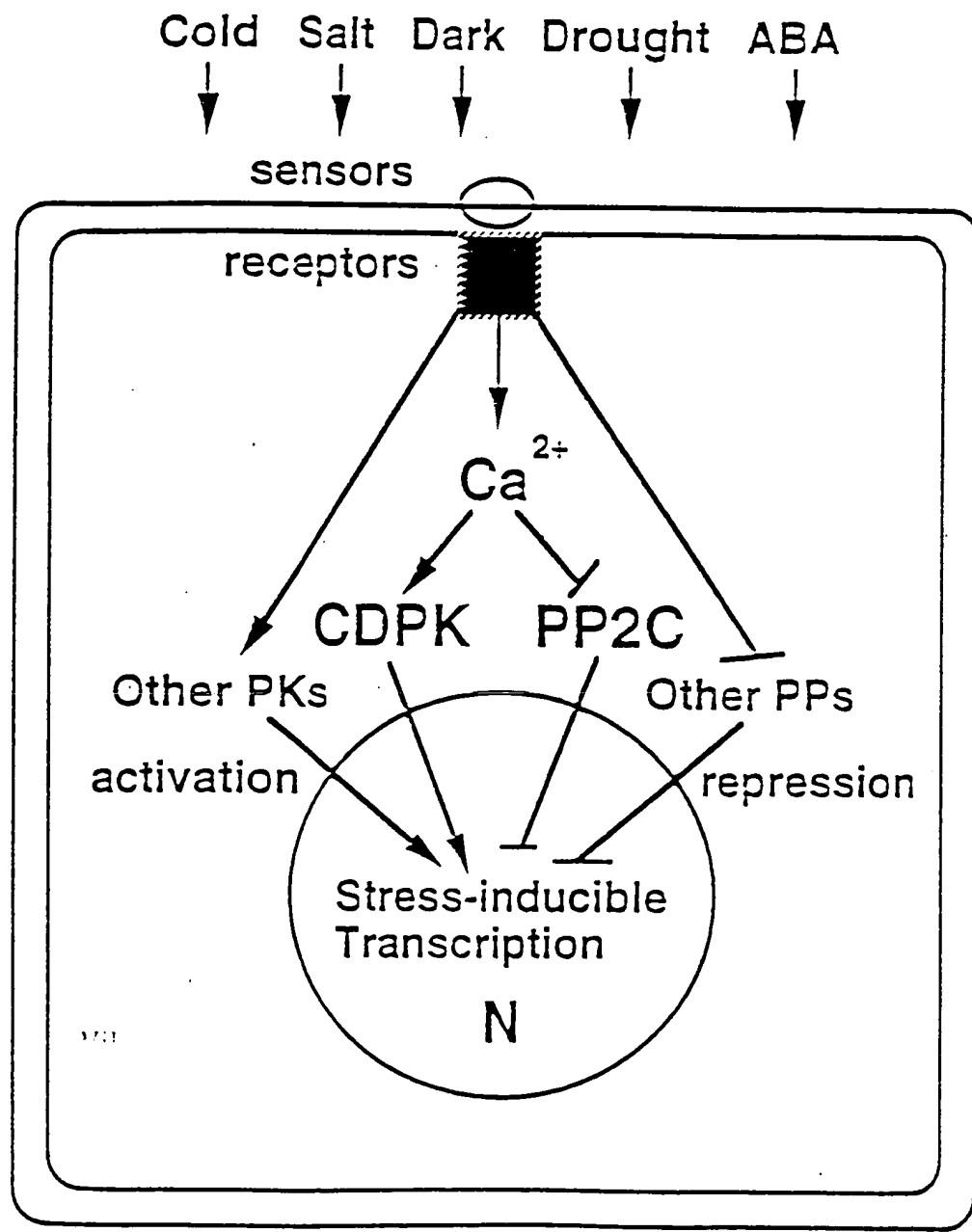


FIG. 4D

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FIGURE 5 (SHEET 1/4)

SEQ ID NO: 1 ↗
1 GTTGTAAACGACGGNCAGTCATTGTAATCGACTCNCTATAGGGCGNAATTGGAGCTC
CAACATTTTGCTGCCNGTCACTTAACATTATGCTGAGNGATATCCCGCTAACCTCGAG 60

a

61 CACCGCGGTGGCGGCCGCTCTAGAAGCTAGTGGATCCATGGCTAACTCAAACTCAGATCAGC
GTGGCGCCACCGCCCGCGAGATCTTGATCACCTAGGTACCCATTAGTTTGAGTCTAGTCG 120

SEQ ID NO: 2 ↗ M A N Q T Q I S -

121 GACAAGTACATCTTAGGACGGAGAACTCGTCGGCGAATTCCGAATCAGTATCTTTGT
CTGTTCATGTAGAATCCTGCTCTTGAGCCAGCGCCGCTTAAGCCTTAGTGCATAGAAC 180

a ~ D K Y I L G R E L G R G E F G I T Y L C -

FIGURE 5 (SHEET 2/4)

030606031-12012697

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ACAGATAGAGAGACTCGTGAAGCTTTAGCTTCAAATCAATCTCAAGAGAAAGCTCCGA 240
181 -----+-----+-----+-----+
TGTCTATCTCTGAGCCTTCGAAATCGAACGTTAGTTAGAGGTTCTCTTCGAGGCT

. T D R E T R E A L A C K S I S K R K L R -
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ACCGCCCTCGATGTGAAAGACGTCCGTGAAAGTCACGATCATGTCACCTTACCGGAA 300
241 -----+-----+-----+-----+
TGGCGGCAGCTACACCTTCTGCAGGCAGCAGTCAGTGCTAGTACAGTTGAAATGGCCTT

. T A V D V E D V R R E V T I M S T L P E -
```



```

CACCCAACGTTGTGAAACTTAAGCGACTTATGAGGATAACGAGACCGTGCATTTGTG 360
301 -----+-----+-----+-----+
GTGGGTTTGCACACTTGAATTTCGCTGAATACTCTTATTCGCTCTGGCACCTAGAACAC

. H P N V V K L K A T Y E D N E T V H L V -
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ATGGAGCTTGAGGAGGTGAGCTTTTGGTCGGATTGTTGCAAGAGGACATTATACA 420
361 -----+-----+-----+-----+
TACCTCGAAACACTCCACTCGAAAACCAGCCTAACACGTTCTCTGTAAATATGT

. M E L C E G G E L F G R I V A R G H Y T -
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17.1


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GAGCGTGGCGGGCGCTACCGTCGGAGAACGATCGGGAAAGTTGTGAGGATGTGTCATGTC 480
421 -----+-----+-----+-----+
CTCGCACGCCGCCATCGCAGCGCTTGTAGGGCTTCAACACTCTACACAGTACAG

. E R A A A T V A R T I A E V V R M C H V -
```

FIGURE 5 (SHEET 3/4)

a . N G V M H R D L K P E N F L F A N K K E -
 481 AATGGTGTTATGCATAGAGATTGAGCTGAGAATTCTTGTGCTAACAGAAGGAG
 TTACCAACAATACTATCTCTAAACTCGGACTCTAAAGAACAAACGATTGTTCTTCCTC
 a N S A L K A I D F G L S V L F K P G E R -
 541 // AATTCTGCACTTAGGCTATTGATTTGGTTATCTGTTCTCTTAAACCTGGAGAGAGG
 TTAAGACGTGAATTCCGATAACTRAACCAAATAGACAGAGAAATTGGACCTCTCTCC
 a F T E I V G S P Y V M A P E V L K R N Y -
 601 TTTACAGAGATTGGAAAGTCCTTATTATATGGCTCCAGAACTGTTGAAAGAGAATTAT
 AAATGTCCTCTAACACCTTCAGGAATAATACCGAGGTCTCACAACTTCTCTTAAATA
 a G P E V D V W S A G V I L Y I L L C G V -
 661 GGACCAGAGGTTCATGTGTGGAGTGCTGGAGTTATCCTCTACATCTTGCTTGTGGTGT
 CCTGGTCTCCAACCTACACACCTCACGACCTCAATAGGAGATGTAGAACCAAACACCAA
 a

FIGURE 5 (SHEET 4/4)

721 CCTCCGTTTGGCCAGAGACTGAACAGGTGTGGCTTGCCATTCAGGGAGTTCTT
 GGAGGC~~AAAACCCG~~TCTGACTTGTCCACACCGAGAACGGT~~AGAA~~CTCCCCTCAAGAA
 P P F W A E T E Q G V A L A I L R G V L -

781 GATTAAAGAGAGATCCTTGGTCGCAGATATCAGAGAGCGCAAAGAGCCTTGTGAAGCAG
 CTAAAATTCTCTAGGAACCAGCGTCTATAGTCCTCGCGTTCTCGGAACACTTCCGTC
 D F K R D P W S Q I S E S A K S L V K Q -

841 ATGTTGGAACCTGATTCAACTAAGCGTTGACTGCTCAGCAAGTTCTGATCACCCCTTGG
 TACAACCTTGGACTAAGTTGATTGCAACTGACCGAGTCGTTCAAGAACTAGTGGAAACC
 M L E P D S T K R L T A Q Q V L D H P W -

901 ATACAGAAATGCAAAGAA~~AGGATCAAC~~CTTATCGATA~~CCGAC~~CTGGACGGGGGGGGGG
 TATGTCTTACGTTCTTCTAGTTGCAATAGCTATGGCAGCTGGAGCTCCCCGGGG
 I Q N A K K

961 CGTACCAAGCTTNGTCCCTT~~TA~~GTGAGGGTTAATTTCGAGCTGGCGTAATCATGTCAT
 CCATGGTCGAAANC~~AAGGAA~~ATC~~ACT~~CCAA~~TT~~AAAGCTCGAACCCATTAGTACAGTA